

**This Page Is Inserted by IFW Operations
and is not a part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- **BLACK BORDERS**
- **TEXT CUT OFF AT TOP, BOTTOM OR SIDES**
- **FADED TEXT**
- **ILLEGIBLE TEXT**
- **SKEWED/SLANTED IMAGES**
- **COLORED PHOTOS**
- **BLACK OR VERY BLACK AND WHITE DARK PHOTOS**
- **GRAY SCALE DOCUMENTS**

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

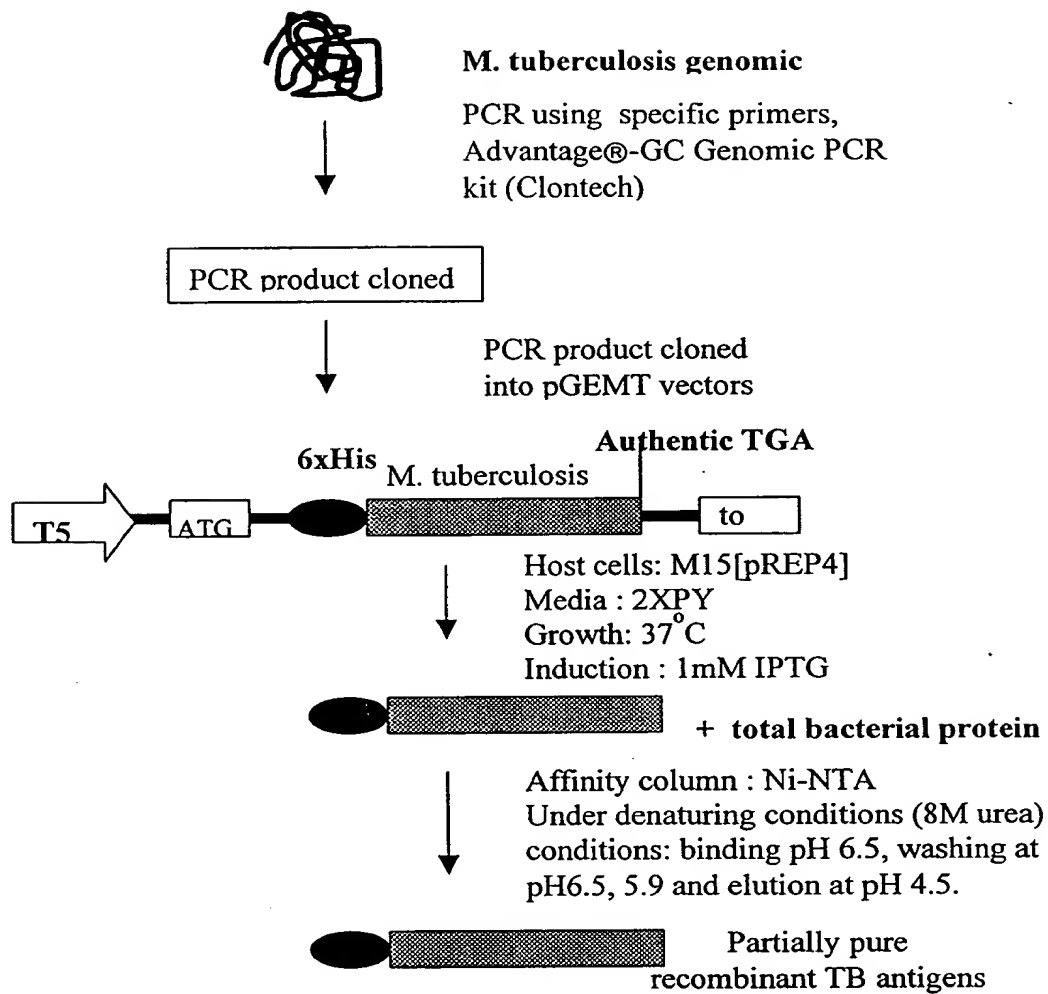
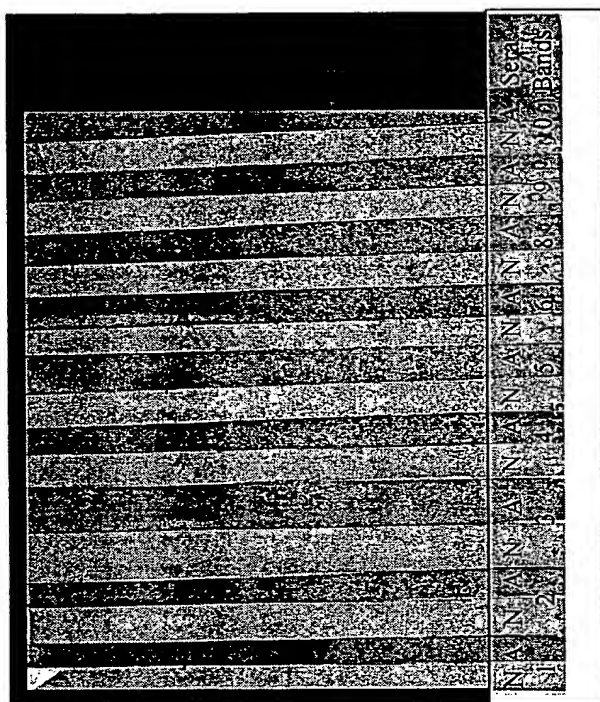


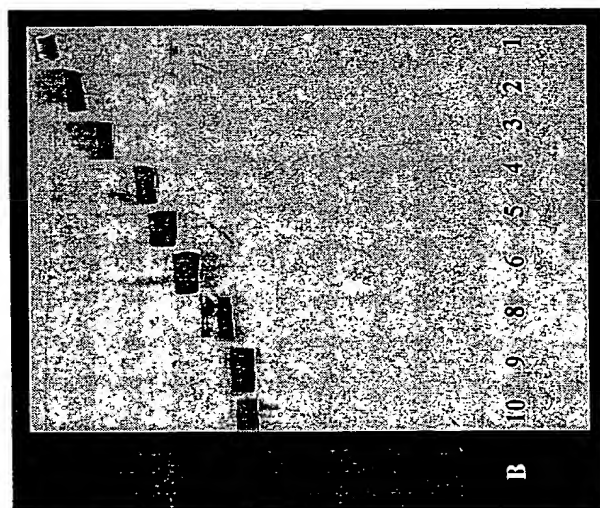
Fig.1 Strategy for the isolation and expression of *M. tuberculosis* protein antigens.

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

- 2/9 -



(B)



(A)

Fig.2. (A) Gel purified and concentrated *M. tuberculosis* protein bands (B.1, 2, 3, 4, 5, 6, 8, 9, 10) blotted onto PVDF membrane were excised for N-terminal sequencing. (B) Concentrated *M. tuberculosis* protein bands blotted onto nitrocellulose membrane and immuno-screened using pooled normal (N) and active (A) sera respectively. Positive bands (arrows) were observed with A but not with N.

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

- 3/9 -

Fig. 3 Result of homology search against the GenBank protein sequence databases. Proteins showing the highest homology to the *M. tuberculosis* protein bands are as shown.

Relative molecular weight (kDa)	Sequence from N-terminal sequencing	Match (GenBank)
B.4	SKLIEYDELALEAME	db: ₂ SKLIEYDETRHAME ₁₆ 55.74kDa, groEL1/protein cpn60 [16], pID=g44601, X60350 (80% match)
B.5	AKTIA YDEEARV	db: ₂ AKTIA YDEEA ₁₀ 56.728 kDa, CHAPERONIN2, groEL2, GenBank pID=g15000, MTTCWPA_3 (100% match)
B.6	AEVDAYKFDPAVD	db: ₁₆₁ AEFDA YRRDPMA ₁₇₂ Probable exported protease, has signal sequence, very similar to three proteases / peptidases from Streptomyces, pID=e235164, MTCY427.04c (51% match)
B.9	AEYTLPLDWDYG	db: ₂ AEYTLPLDWDYG ₁₄ 23.0 kDa, superoxide dismutase, pID=g581379, MTSOD4 (100% match)
B.10	MEIDILAVAAP	db: ₁₁₇ IEVDLLDLAP ₁₂₇ 33 kDa, mycocerosic acid synthase [17], pID=g149978, M95808 (56.9% match)
MMP	ATTLPVQRHDARL	db: ATLPVQRHPSL 14/16 kDa [18], pID=g244562, M76712

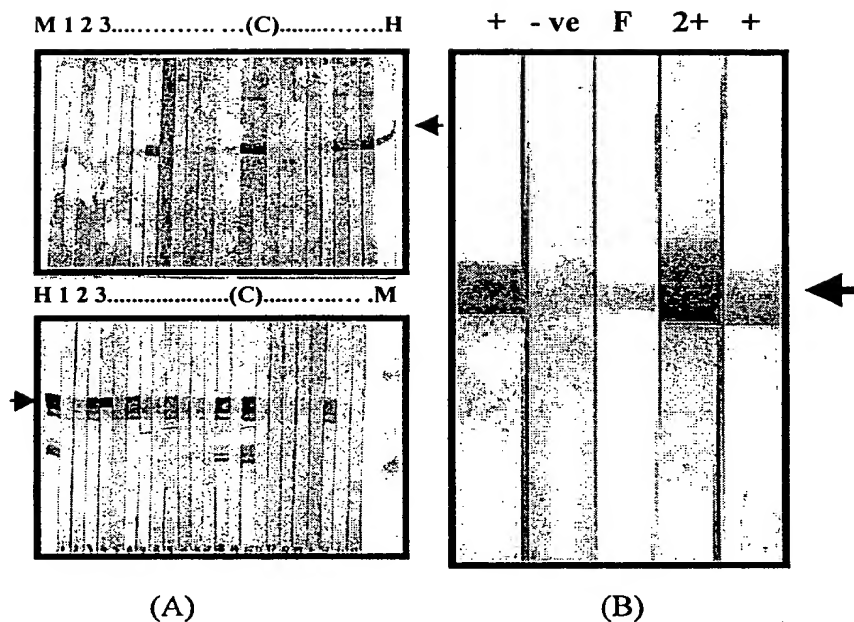


Fig. 4. Western screening of recombinant *M. tuberculosis* antigens. (A) Arrows indicate the position of the recombinant antigens on the membrane. M= Kaleidoscope protein Marker and H= strip probed with anti-RGSHis, C= a positive control of strips probed with known human serum reactive to the specific recombinant antigen. (B) Reactivity is estimated based on the intensity of band on

Fig 5. Percentage of reactivity of recombinant TB antigens against different sera panels. A known 38kDa antigen [20, 21] of *M. tuberculosis* was included in the screening. The gene (GeneBank Accession # M30046) for this antigen was cloned, expressed in pQE30 and partially purified as described in section E. Also shown are the percentage of reactivity of sera samples detected by a commercially available rapid TB diagnostic kit from ICT (Amrad).

Panel:	Sera	Uninfected (normal)	Active TB (Extra-Pulmonary)	Active TB (Pulmonary)	Inactive
Recombinant antigens:					
B.4		5%	55%	47.8%	22.7%
B.5		25%	35%	39.1%	27.3%
B.6		0%	5%	52.2%	9.1%
B.9		0%	25%	17.4%	18.2%
B.10		0%	5%	26.1%	0%
MMP		0%	25%	8.7%	4.5%
C17		0%	15%	13.0%	4.5%
38 kDa		0%	40%	39.1%	18.2%
ICT TB Kit		0%	55%	52.2%	13.6%

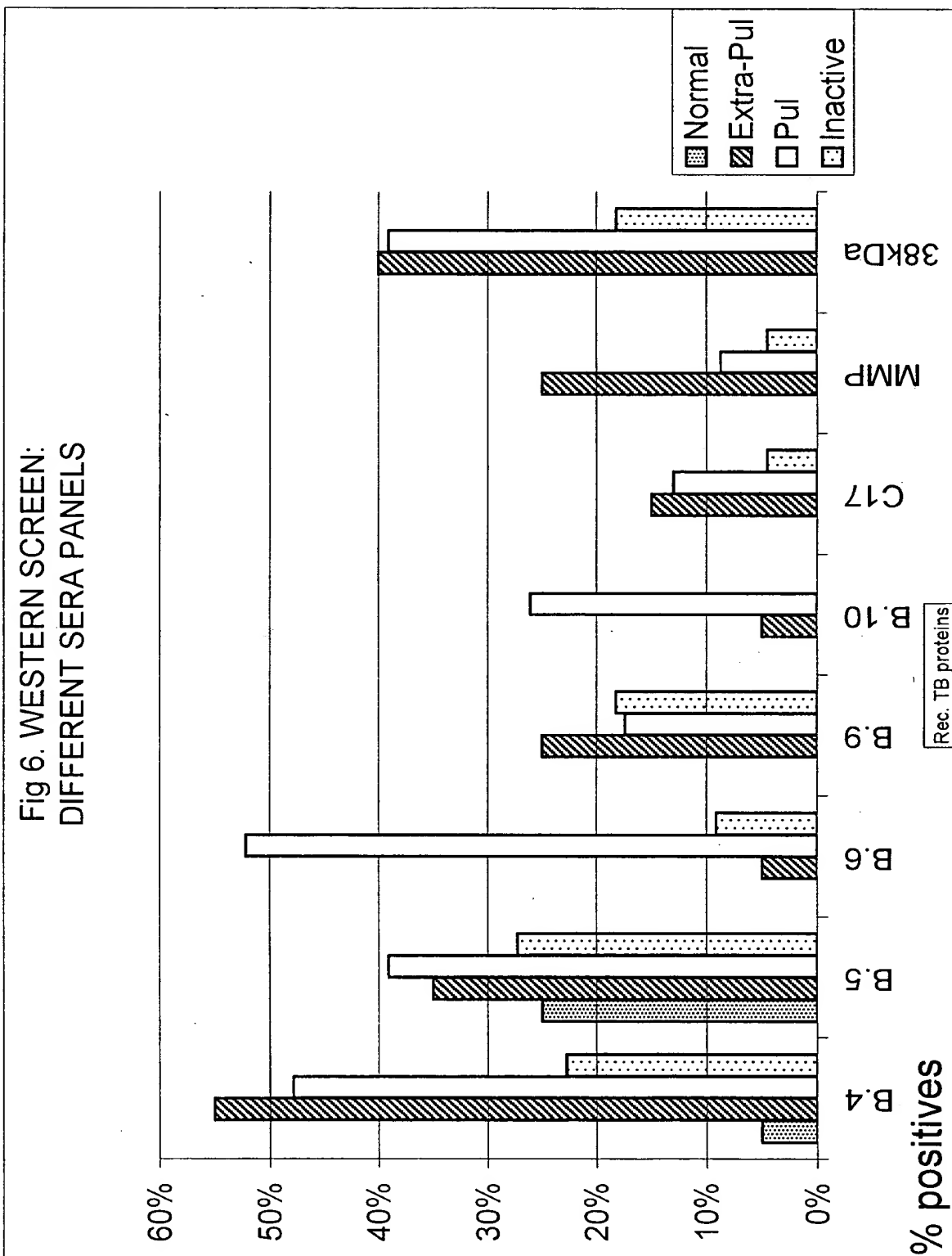


Fig. 7 Sensitivity: Combinations of rec. TB proteins

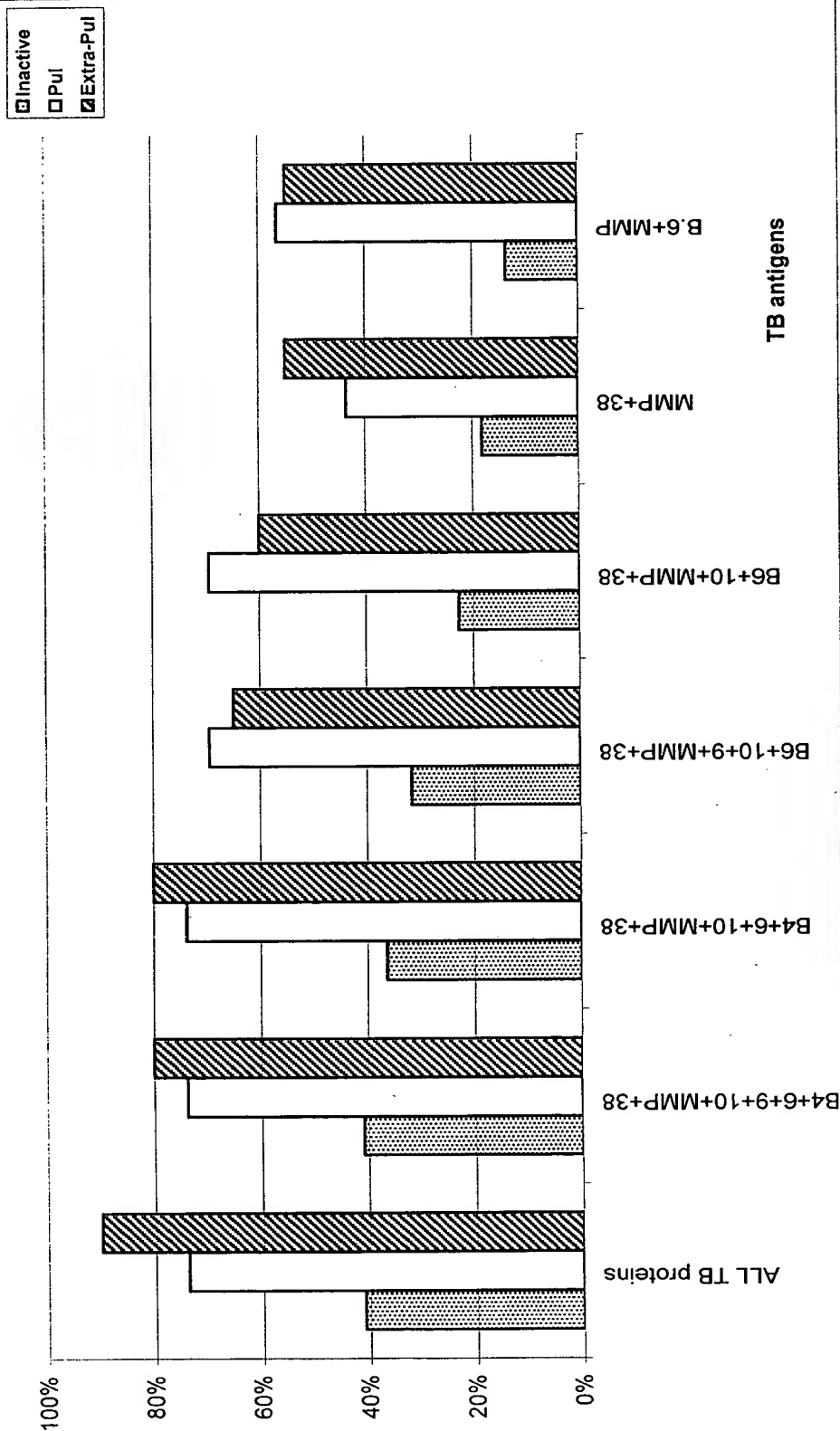


Fig. 8 Comparison of our rec. TB proteins
with the ICT TB diagnostic kit

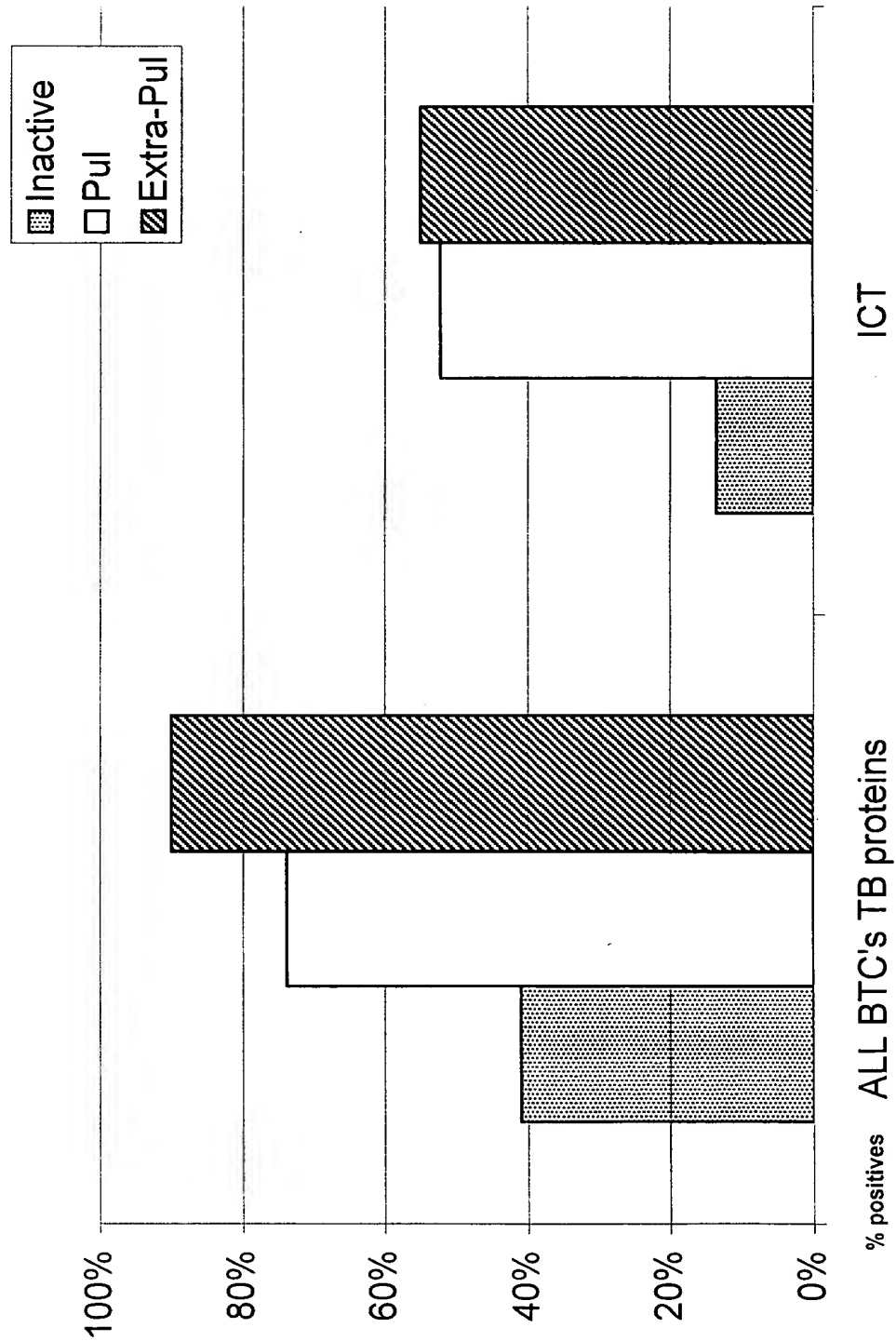


Fig.9 Comparison of combinations of our rec. TB proteins with the ICT kit

